

SEQUENCE LISTING

<110> Union Chimique Belge, S.A.
Nocka, Karl
Pirozzi, Gregory
Einstein, Richard

<120> NOVEL GENES ASSOCIATED WITH ALLERGIC HYPERSENSITIVITY AND MAST CELL ACTIVATION

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<170> PatentIn version 3.1

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HOMO SAPIENS

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Glu Glu Val Cys Tyr Thr Val Ile Asn His Ile Pro His Gln Arg Ser
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16005302 - 16005302

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2020-2021

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Leu Cys Pro Gly Ser Cys Leu Glu Gly Glu Val Val Cys Trp Glu Gly
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Ile Ala Gly Gln Glu Gly Asp Pro Gly Leu Arg Gly His Thr Lys Arg
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Lys Lys Arg Ile Pro Arg Thr Tyr Pro Ser His Leu Trp Ile Pro Gly
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Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro
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Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu
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Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala
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Pro Ser Leu Ser Pro His Cys Cys Pro Cys Gln Ala Leu Ser Leu Glu
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TOXICITY PROTEIN

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His Leu His Pro Arg Ser Ala Gly Pro Leu Pro Val Met Ser Pro Tyr
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tgg agc gga ggc ttc tac agc aac cgc agc ctc gcc ctc gtc atg agc Trp Ser Gly Gly Phe Tyr Ser Asn Arg Ser Leu Ala Leu Val Met Ser 190 195 200	988
cag gcc cgc ttc gag aag atc ctc aag tac ttc cac gtc gtg gcc ttc Gln Ala Arg Phe Glu Lys Ile Leu Lys Tyr Phe His Val Val Ala Phe 205 210 215 220	1036
cgc tcc agc cag acc acg cac ggg ctc tac aag gtc cag ccc ttc ctc Arg Ser Ser Gln Thr Thr His Gly Leu Tyr Lys Val Gln Pro Phe Leu 225 230 235	1084
gac tcc ctg cag aac agc ttc gac tct gcc ttc agg cct tcc caa acc Asp Ser Leu Gln Asn Ser Phe Asp Ser Ala Phe Arg Pro Ser Gln Thr 240 245 250	1132
cag gtg cta cat gaa ccc ctg atc gat gag gat cct gta ttc att gcc Gln Val Leu His Glu Pro Leu Ile Asp Glu Asp Pro Val Phe Ile Ala 255 260 265	1180

acg tgc aca gag cgg gag ctg cga aag agg aaa aag cgg aaa ttc agc Thr Cys Thr Glu Arg Glu Leu Arg Lys Arg Lys Lys Arg Lys Phe Ser 270	275	280	1228
ctc tgg gtc aga caa tgt tct tcc act ggc ttc atc atc cag att tat Leu Trp Val Arg Gln Cys Ser Ser Thr Gly Phe Ile Ile Gln Ile Tyr 285	290	295	300
gtc cac ctg aag gaa ggt ggg ggc cca gat ggc ctg gat gcg ctg aag Val His Leu Lys Glu Gly Gly Pro Asp Gly Leu Asp Ala Leu Lys 305	310	315	1324
aat aag ccc cag ctc cac agc atg gtg gcc agg agc ctg tgc cgg aac Asn Lys Pro Gln Leu His Ser Met Val Ala Arg Ser Leu Cys Arg Asn 320	325	330	1372
gcg gca ggc aag aac tac atc att ttc acg ggg ccc agc atc acc agc Ala Ala Gly Lys Asn Tyr Ile Ile Phe Thr Gly Pro Ser Ile Thr Ser 335	340	345	1420
ctg acg ctg ttt gaa gag ttt gag aag caa ggg att tac tgc tgc ggc Leu Thr Leu Phe Glu Glu Phe Glu Lys Gln Gly Ile Tyr Cys Cys Gly 350	355	360	1468
ttg ctc cgc cgcc aag agt gac tgc acc ggc ctc cca ctg tcc atg Leu Leu Arg Ala Arg Lys Ser Asp Cys Thr Gly Leu Pro Leu Ser Met 365	370	375	1516
ctg acc aac cca gcc aca ccc ccg gcc cgg ggc cag tac caa atc aag Leu Thr Asn Pro Ala Thr Pro Pro Ala Arg Gly Gln Tyr Gln Ile Lys 385	390	395	1564
atg aag ggg aac atg tcc ttg atc tgc tgg tac aac aaa gga cac ttc Met Lys Gly Asn Met Ser Leu Ile Cys Trp Tyr Asn Lys Gly His Phe 400	405	410	1612
cgc ttc ctg acc aac gcc tac tcc ccg gtg cag cag gga gtc atc atc Arg Phe Leu Thr Asn Ala Tyr Ser Pro Val Gln Gln Gly Val Ile Ile 415	420	425	1660
aaa agg aag agt ggg gag atc cca tgc ccc ttg gcc gtg gag gcg ttt Lys Arg Lys Ser Gly Glu Ile Pro Cys Pro Leu Ala Val Glu Ala Phe 430	435	440	1708
gcc gct cac ctg agc tac atc tgc aga tac gat gac aaa tac agc aag Ala Ala His Leu Ser Tyr Ile Cys Arg Tyr Asp Asp Lys Tyr Ser Lys 445	450	455	1756
tat ttc att tct cat aaa cca aac aag acc tgg cag cag gtg ttc tgg Tyr Phe Ile Ser His Lys Pro Asn Lys Thr Trp Gln Gln Val Phe Trp 465	470	475	1804
ttc gcc atc agc atc gcc atc aac aat gcc tac atc ctg tac aaa atg Phe Ala Ile Ser Ile Ala Ile Asn Asn Ala Tyr Ile Leu Tyr Lys Met 480	485	490	1852
tca gac gcc tac cac gtg aag agg tac agc cgg gcg cag ttt gga gag Ser Asp Ala Tyr His Val Lys Arg Tyr Ser Arg Ala Gln Phe Gly Glu 495	500	505	1900
aga ctc gtc aga gag ctg ctg ggc ttg gag gat gcc tct ccg acc cac			1948

2000-2001

Arg Leu Val Arg Glu Leu Leu Gly Leu Glu Asp Ala Ser Pro Thr His
510 515 520

tga tgctggggc gcaggactcg gtcaagggag gggcaagagg aggaggagag	2001
cctgccgttc caacttgcacc atcagagacc cggacacggc ctggtgtgtg gcttgctgcc	2061
tgggagggat gcacagggcc tctggagggc caggatggac ctggtcagag gacggttgct	2121
gtcctcattt gcattccaag aagagcatgt cctccctcga gaaacagtgc cgccgggtgt	2181
atgagcactt acacccacgt tctcaagggc agattctctc atgacatccg tggagcttgc	2241
gaggcagcgt ggactggta ctgtgaagga aggccccgt ggtagaatga gctggagcac	2301
gctctaagag agatgcctgc ttccctaaaga tctacagcaa tctggacgt gttcaagtt	2361
caagacttga aggaagcaaa gacgcctgc atggttacaa tggctcaggt gtcagggag	2421
gccggagggt ttccagcat ttgcctcatg ccagcacctt tgaaccggtc tcttagaaga	2481
agacacacat cctgggtgta cagtggtaa atggggagtg ggtgcccatt ctgaaaaacg	2541
aggcattcct gtcattccc tctgcttagc tggtgccag gggagagagg gaaatgcca	2601
aaacttggag tgaaggatga tgctatTTT tATTTAA tatatcttca gttatTTT	2661
ttactgttgc ttcaGatcta atgtaaaagg cagatgtccc ctcccttcca ccccccacgc	2721
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aggccggga agggccgctg gctccgaac agacgtggtt gctctccacg aggccatgg	2841
ggagcccgcg ggcctaagc tttgtcgacg atgtcatcat tggcagaatt acttgtttg	2901
aaaaataagt agcattgctg aaacacacaa ccgaattctc tacgatggcc atttgctcat	2961
tgtctttct ctgtgtgt tag tgagtgaccc tggcagtgtt tgctgctca gagtgcccc	3021
tcagaacaac agggctggcc ttggaaaaac cccaaaacag gactgtggtg acactctgg	3081
tcaggtgtga ttgacatga gggccggagg cgggtgctga cggcaggact ggagaggctg	3141
cgtccccggc actggcagcg aggctcggt gtccccagg cagatctggg cactttccca	3201
acccaggttt atgcgtctcc agggaaagct cggtgccaga gtggtggca gatctgacca	3261
tccccacaga ccagaaacaa ggaatttctg ggattaccca gtcccccttc aacccagttg	3321
atgttaaccac ctcatTTT acaaatacag aatctattct actcaggcta tggcctcgt	3381
cctcaactcag ttattgcgag tggcgtgtc cgcattgtcc gggccccacg tggctcctgt	3441
gctctagatc atggtgactc cccgcctg tggttggat cgatgccacg gattgcaggc	3501
caaatttcag atcggtttc caaacacct tgcgtgccc ttatggaa ttgaaagcac	3561
ttttaccaca tggagaaata tattttat ttgtgtatgt tttctacaag gtccactatt	3621
tctgagtttta atgtgtttcc aacacttaag gagactctaa tgaaagctga tgaattttct	3681

tttctgtcca aacaagtaaa ataaaaataa aagtctattt agatgttaaa aaaaaaaaaa 3741
aa 3743

<210> 7
<211> 524
<212> PRT
<213> Homo sapiens

<400> 7

Met Ala Glu Gly Gly Gly Ala Arg Arg Arg Ala Pro Ala Leu Leu
1 5 10 15

Glu Ala Ala Arg Ala Arg Tyr Glu Ser Leu His Ile Ser Asp Asp Val
20 25 30

Phe Gly Glu Ser Gly Pro Asp Ser Gly Gly Asn Pro Phe Tyr Ser Thr
35 40 45

Ser Ala Ala Ser Arg Ser Ser Ala Ala Ser Ser Asp Asp Glu Arg
50 55 60

Glu Pro Pro Gly Pro Pro Gly Ala Ala Pro Pro Pro Pro Arg Ala Pro
65 70 75 80

Asp Ala Gln Glu Pro Glu Glu Asp Glu Ala Gly Ala Gly Trp Ser Ala
85 90 95

Ala Leu Arg Asp Arg Pro Pro Arg Phe Glu Asp Thr Gly Gly Pro
100 105 110

Thr Arg Lys Met Pro Pro Ser Ala Ser Ala Val Asp Phe Phe Gln Leu
115 120 125

Phe Val Pro Asp Asn Val Leu Lys Asn Met Val Val Gln Thr Asn Met
130 135 140

Tyr Ala Lys Lys Phe Gln Glu Arg Phe Gly Ser Asp Gly Ala Trp Val
145 150 155 160

Glu Val Thr Leu Thr Glu Met Lys Ala Phe Leu Gly Tyr Met Ile Ser
165 170 175

Thr Ser Ile Ser His Cys Glu Ser Val Leu Ser Ile Trp Ser Gly Gly
180 185 190

Phe Tyr Ser Asn Arg Ser Leu Ala Leu Val Met Ser Gln Ala Arg Phe

195

200

205

Glu Lys Ile Leu Lys Tyr Phe His Val Val Ala Phe Arg Ser Ser Gln
210 215 220

Thr Thr His Gly Leu Tyr Lys Val Gln Pro Phe Leu Asp Ser Leu Gln
225 230 235 240

Asn Ser Phe Asp Ser Ala Phe Arg Pro Ser Gln Thr Gln Val Leu His
245 250 255

Glu Pro Leu Ile Asp Glu Asp Pro Val Phe Ile Ala Thr Cys Thr Glu
 260 265 270

Arg Glu Leu Arg Lys Arg Lys Lys Arg Lys Phe Ser Leu Trp Val Arg
275 280 285

Gln Cys Ser Ser Thr Gly Phe Ile Ile Gln Ile Tyr Val His Leu Lys
290 295 300

Glu Gly Gly Gly Pro Asp Gly Leu Asp Ala Leu Lys Asn Lys Pro Gln
305 310 315 320

Leu His Ser Met Val Ala Arg Ser Leu Cys Arg Asn Ala Ala Gly Lys
325 330 335

Asn	Tyr	Ile	Ile	Phe	Thr	Gly	Pro	Ser	Ile	Thr	Ser	Leu	Thr	Leu	Phe
340									345						350

Glu Glu Phe Glu Lys Gln Gly Ile Tyr Cys Cys Gly Leu Leu Arg Ala
355 360 365

Arg Lys Ser Asp Cys Thr Gly Leu Pro Leu Ser Met Leu Thr Asn Pro
370 375 380

Ala Thr Pro Pro Ala Arg Gly Gln Tyr Gln Ile Lys Met Lys Gly Asn
385 390 395 400

Met Ser Leu Ile Cys Trp Tyr Asn Lys Gly His Phe Arg Phe Leu Thr
405 410 415

Asn Ala Tyr Ser Pro Val Gln Gln Gly Val Ile Ile Lys Arg Lys Ser
 420 425 430

Gly Glu Ile Pro Cys Pro Leu Ala Val Glu Ala Phe Ala Ala His Leu
435 440 445

FOODS FOR LIFE

Ser Tyr Ile Cys Arg Tyr Asp Asp Lys Tyr Ser Lys Tyr Phe Ile Ser
450 455 460

His Lys Pro Asn Lys Thr Trp Gln Gln Val Phe Trp Phe Ala Ile Ser
465 470 475 480

Ile Ala Ile Asn Asn Ala Tyr Ile Leu Tyr Lys Met Ser Asp Ala Tyr
485 490 495

His Val Lys Arg Tyr Ser Arg Ala Gln Phe Gly Glu Arg Leu Val Arg
500 505 510

Glu Leu Leu Gly Leu Glu Asp Ala Ser Pro Thr His
515 520

<210> 8
<211> 1998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (162)..(635)
<223> 1st open reading frame .

<400> 8
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gcttccaaac tcattttga ataatactag gctacaaaga attacactgt gaattcatta 120
aggtaaacac caaatcacta aacagcactg tttgtacaga a atg tcg aaa agc tgt 176
Met Ser Lys Ser Cys
1 5

gga aat aat tta gcg gcc att tct gta gga att tcg ctt ctt tta ctc 224
Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile Ser Leu Leu Leu
10 15 20

tta gtg gtt tgt gga att ggg tgt gtt tgg cac tgg aaa cac cgt gtt 272
Leu Val Val Cys Gly Ile Gly Cys Val Trp His Trp Lys His Arg Val
25 30 35

gcc aca cga ttt acc tta ccg agg ttt tta caa agg aga agc agc agg 320
Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln Arg Arg Ser Ser Arg
40 45 50

aga aaa gtc tgt act aaa aca ttc ttg ggc ccc cgc atc att ggc tta 368
Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro Arg Ile Ile Gly Leu
55 60 65

agg cat gaa atc tca gtt gaa acc caa gac cac aaa tct gct gtc agg 416
Arg His Glu Ile Ser Val Glu Thr Gln Asp His Lys Ser Ala Val Arg
70 75 80 85

KODAK SAFETY FILM

gga aat aac aca cac gac aac tat gaa aat gtg gaa gca ggt cct ccc Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val Glu Ala Gly Pro Pro 90 95 100	464
aaa gct aaa gga aaa acc gat aag gaa cta tat gaa aac aca ggg cag Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr Glu Asn Thr Gly Gln 105 110 115	512
tct aat ttc gag gag cat atc tat gga aat gag aca tct tct gac tat Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu Thr Ser Ser Asp Tyr 120 125 130	560
tat aac ttc cag aag cct cgt cct tct gaa gtt cct caa gat gaa gat Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val Pro Gln Asp Glu Asp 135 140 145	608
ata tac att ctt cca gat tca tat tag cttttcaaaa tattgacttt Ile Tyr Ile Leu Pro Asp Ser Tyr 150 155	655
tgttattgga tgataaatat tcactgtaat ttttcaacag caaagacaag gaatcaaact aaatgttgat caactgtaga ctggataaaag aaaatgtggt acacatacac catagaatat tatgcagccg taaaaaaaaa acaaaaactaa catgggaaca gaaaatcaaa taccacatat tctcacttaa aagtgggagc taaataataa gaacacatgg agagaaggag aggaacaaca gacactgggg cctacttgag ggaggacagt ggaaggaggg agaggttcag ggaaaaaaaaa aatatcaggt actatgctta gtacacacat gatgaaataa tctgtacacc aaacccccaa gtcacaagtg ttcctacata acaaacctga acatgtaccc ctgaacataa aattataatt aaaatattaa aaataattca ctgtgatttt tattgtactg atgccattct taatcaagtt ctgataagtg gatggctct gcctatctcc acctttctga atcctatgtg tatkctgt gattaattct agatatcttc tccaccctcc ttgcaccaga ctaaatctgt attatgtgat attgattctt ccttctaaat attaccggtt atctcttcc tttatttcta ccattatctt tatctggctc agaattattg tcataggctc ctaactgttc ctccctgcttc tagttctac ccactcaatc aattaccgat ggtgttgcga gatttatctt cagaaaaatat tcctaacagc cacattattt ctttcaactta aaatgtttta atgccccctc tttgcaaaag acataatacc cataatttga actccaaaat ttatggtttt ccacaattgg ttccaattca cttttccagt gacttctctt actatctctc atttctttgc cttagcaga atcatcttaa aacctgccaa acttattcctt cttcacagc tttgcttttc tgccctttct ctcaagcctg cttcagatca taagttcttc cacacatctc ctgaatcact ccaaaccgc atttaccttt ttatTTCTG atataagctt tcatggctct tcaattctta ggacatttaa acatatgaat gttgccacag cattttattta cctagcttca tatgaaaaatg tcttaaattc ccacctaaat gaaaagaaac	715 775 835 895 955 1015 1075 1135 1195 1255 1315 1375 1435 1495 1555 1615 1675 1735 1795 1855

tgcccaaatg cctagaacat cacataaggc actaaatgcc tcatgttta ctgacggaa 1915
ttgaattgta catttgctg agtagtttg agaaaaaaat ctaataaatt catctgttat 1975
tcatccataa aaaaaaaaaaaa aaa 1998

<210> 9
<211> 157
<212> PRT
<213> Homo sapiens

<400> 9

Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile
1 5 10 15

Ser Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His
20 25 30

Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln
35 40 45

Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro
50 55 60

Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His
65 70 75 80

Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val
85 90 95

Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr
100 105 110

Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu
115 120 125

Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val
130 135 140

Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr
145 150 155

<210> 10
<211> 1998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (373)..(651)
<223> 2nd open reading frame

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aggtaaacac caaatcacta aacagcaactg tttgtacaga aatgtcgaaa agctgtggaa 180
ataatttagc ggcatttct gtaggaattt cgcttctttt actcttagtg gtttgtggaa 240
ttgggtgtgt ttggcactgg aaacaccgtg ttgccacacg atttacctta ccgaggtttt 300
tacaaaggag aagcagcagg agaaaaagtct gtactaaaac attcttggc cccgcacca 360
ttggcttaag gc atg aaa tct cag ttg aaa ccc aag acc aca aat ctg ctg 411
Met Lys Ser Gln Leu Lys Pro Lys Thr Thr Asn Leu Leu
1 5 10
tca ggg gaa ata aca cac acg aca act atg aaa atg tgg aag cag gtc 459
Ser Gly Glu Ile Thr His Thr Thr Met Lys Met Trp Lys Gln Val
15 20 25
ctc cca aag cta aag gaa aaa ccg ata agg aac tat atg aaa aca cag 507
Leu Pro Lys Leu Lys Glu Lys Pro Ile Arg Asn Tyr Met Lys Thr Gln
30 35 40 45
ggc agt cta att tcg agg agc ata tct atg gaa atg aga cat ctt ctg 555
Gly Ser Leu Ile Ser Arg Ser Ile Ser Met Glu Met Arg His Leu Leu
50 55 60
act att ata act tcc aga agc ctc gtc ctt ctg aag ttc ctc aag atg 603
Thr Ile Ile Thr Ser Arg Ser Leu Val Leu Leu Lys Phe Leu Lys Met
65 70 75
aag ata tat aca ttc ttc cag att cat att agc ttt tca aaa tat tga 651
Lys Ile Tyr Thr Phe Phe Gln Ile His Ile Ser Phe Ser Lys Tyr
80 85 90
ctttgttat tggatgataa atattcaactg taattttca acagcaaaga caaggaatca 711
aactaaatgt tgatcaactg tagactggat aaagaaaatg tggcacat acaccataga 771
atattatgca gccgtaaaaa aagaacaaaa ctaacatggg aacagaaaat caaataccac 831
atattctcac ttaaaagtgg gagctaaata ataagaacac atggagagaa ggagaggaac 891
aacagacact gggcctact tgagggagga cagtggagg aggagaggt tcagggaaaa 951
aaaaaatatc aggtactatg ctttgtacac acatgtgaa ataatctgta caccaaaccc 1011
ccaagtcaca agtgttccta cataacaaac ctgaacatgt accctgaac ataaaattat 1071
aattaaaata ttaaaataa ttcaactgtga ttttattgt actgatgcca ttcttaatca 1131
agttctgata agtggatggt ctctgcctat ctccacctt ctgaatccta tgtgtatcgc 1191
tgtggattaa ttcttagatat cttctccacc ctcccttgcac cagactaaat ctgtattatg 1251

2000-2001

tgatatttgc tcttccttct aaatatttacc cgtttatctct ttccttttatt tctaccatta 1311
tctttatctg gtcagaatt attgtcatag gtcctaact gttccttcctg cttcttagttt 1371
ctacccactc aatcaattac cgatgggttt gccagattta tcttcagaaa atattcctaa 1431
cagccacatt atttcttca cttaaaatgt tttaatgccc cctcttgca aaagacataa 1491
tacccataat ttgaactcca aaatttatgg tttccacaa ttgggtccaa ttcactttc 1551
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ccaaacttat ctttccttca cagcttgct tttctgcctc ttctctcaag cctgcttcag 1671
atcataagtt ctccacaca tctcctgaat cactccaaac ccgcatttac ctttttattt 1731
tctgatataa gcttgatgc ctcttcaatt cttaggacat taaaacatat gaatgttgcc 1791
acagcatttt attacctagc ttcatatgaa aatgtcttaa attcccacct aatgaaaag 1851
aaactgcccc aatgcctaga acatcacata aggcactaaa tgcctcatgt tttactgacg 1911
ggaattgaat tgtacatttt gctgagtagt tttgagaaaaaa aatctaata aattcatctg 1971
ttattcatcc ataaaaaaaaaaaaaaa 1998

<210> 11
<211> 92
<212> PRT
<213> Homo sapiens

<400> 11

Met Lys Ser Gln Leu Lys Pro Lys Thr Thr Asn Leu Leu Ser Gly Glu
1 5 10 15

Ile Thr His Thr Thr Met Lys Met Trp Lys Gln Val Leu Pro Lys
20 25 30

Leu Lys Glu Lys Pro Ile Arg Asn Tyr Met Lys Thr Gln Gly Ser Leu
35 40 45

Ile Ser Arg Ser Ile Ser Met Glu Met Arg His Leu Leu Thr Ile Ile
50 55 60

Thr Ser Arg Ser Leu Val Leu Leu Lys Phe Leu Lys Met Lys Ile Tyr
65 70 75 80

Thr Phe Phe Gln Ile His Ile Ser Phe Ser Lys Tyr
85 90

<210> 12
<211> 1662
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1662)

<223>

<400>	12			
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1	5	10	15	
cag ctc ttg ctg gtc aac ctg cta acc	ttt ggc ctg gag gtg	tgt ttg		96
Gln Leu Leu Val Asn Leu Leu Thr	Phe Gly Leu Glu Val	Cys Leu		
20	25	30		
gcc gca ggc atc acc tat	gtg ccg cct ctg ctg gaa	gtg ggg gta		144
Ala Ala Gly Ile Thr Tyr Val Pro	Pro Leu Leu Glu Val	Gly Val		
35	40	45		
gag gag aag ttc atg acc atg	gtg ctg ggc att	ggt cca gtg	ctg ggc	192
Glu Glu Lys Phe Met Thr	Met Val Leu Gly Ile	Gly Pro Val	Leu Gly	
50	55	60		
ctg gtc tgt gtc ccg ctc cta	ggc tca gcc agt	gac cac tgg cgt	gga	240
Leu Val Cys Val Pro Leu Leu Gly	Ser Ala Ser Asp His Trp Arg	Gly		
65	70	75	80	
cgc tat ggc cgc cgc ccc	ttc atc tgg gca	ctg tcc ttg	ggc atc	288
Arg Tyr Gly Arg Arg Pro Phe Ile	Trp Ala Leu Ser Leu Gly Ile			
85	90	95		
ctg ctg agc ctc ttt ctc atc	cca agg gcc ggc	tgg cta gca	ggg ctg	336
Leu Leu Ser Leu Phe Leu Ile	Pro Arg Ala Gly Trp Leu	Ala Gly Leu		
100	105	110		
ctg tgc ccg gat ccc agg ccc	ctg gag ctg gca	ctg ctc atc	ctg ggc	384
Leu Cys Pro Asp Pro Arg Pro	Leu Glu Leu Ala Leu	Ile Leu Gly		
115	120	125		
gtg ggg ctg ctg gac ttc	tgt ggc cag gtg	tgc ttc act	cca ctg gag	432
Val Gly Leu Leu Asp Phe	Cys Gly Gln Val Cys	Phe Thr Pro	Leu Glu	
130	135	140		
gcc ctg ctc tct gac ctc	ttc ccg gac cac	tgt cgc cag	gcc	480
Ala Leu Leu Ser Asp Leu Phe	Arg Asp Pro Asp His	Cys Arg Gln	Ala	
145	150	155	160	
tac tct gtc tat	gcc ttc atg atc	agt ctt ggg ggc	tgc ctg ggc tac	528
Tyr Ser Val Tyr Ala Phe Met	Ile Ser Leu Gly	Gly Cys Leu	Gly Tyr	
165	170	175		
ctc ctg cct gcc att	gac tgg gac acc	agt gcc ctg gcc	ccc tac ctg	576
Leu Leu Pro Ala Ile Asp Trp	Asp Thr Ser Ala	Leu Ala Pro	Tyr Leu	
180	185	190		
ggc acc cag gag gag	tgc ctc ttt ggc	ctg ctc acc	ctc atc ttc ctc	624
Gly Thr Gln Glu Glu Cys Leu	Phe Gly Leu Leu	Thr Leu Ile	Phe Leu	
195	200	205		

100056302 - 420202

acc tgc gta gca gcc aca ctg ctg gtg gct gag gag gca gcg ctg ggc			672
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly			
210	215	220	
ccc acc gag cca gca gaa ggg ctg tcg gcc ccc tcc ttg tcg ccc cac			720
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His			
225	230	235	240
tgc tgt cca tgc cgg gcc cgc ttg gct ttc cgg aac ctg ggc gcc ctg			768
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu			
245	250	255	
ctt ccc cgg ctg cac cag ctg tgc cgc atg ccc cgc acc ctg cgc			816
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg			
260	265	270	
cgg ctc ttc gtg gct gag ctg tgc agc tgg atg gca ctc atg acc ttc			864
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe			
275	280	285	
acg ctg ttt tac acg gat ttc gtg ggc gag ggg ctg tac cag ggc gtg			912
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val			
290	295	300	
ccc aga gct gag ccg ggc acc gag gcc cgg aga cac tat gat gaa ggc			960
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly			
305	310	315	320
gtt cgg atg ggc agc ctg ggg ctg ttc ctg cag tgc gcc atc tcc ctg			1008
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu			
325	330	335	
gtc ttc tct ctg gtc atg gac ccg ctg gtg cag cga ttc ggc act cga			1056
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg			
340	345	350	
gca gtc tat ttg gcc agt gtg gca gct ttc cct gtg gct gcc ggt gcc			1104
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala			
355	360	365	
aca tgc ctg tcc cac agt gtg gcc gtg gtg aca gct tca gcc gcc ctc			1152
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu			
370	375	380	
acc ggg ttc acc ttc tca gcc ctg cag atc ctg ccc tac aca ctg gcc			1200
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala			
385	390	395	400
tcc ctc tac cac cgg gag aag cag gtg ttc ctg ccc aaa tac cga ggg			1248
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly			
405	410	415	
gac act gga ggt gct agc agt gag gac agc ctg atg acc agc ttc ctg			1296
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu			
420	425	430	
cca ggc cct aag cct gga gct ccc ttc cct aat gga cac gtg ggt gct			1344
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala			
435	440	445	
gga ggc agt ggc ctg ctc cca cct cca ccc gcg ctc tgc ggg gcc tct			1392

HOMO SAPIENS

Gly	Gly	Ser	Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	
450				455						460						
gcc tgt gat gtc tcc gta cgt gtg gtg ggt gag ccc acc gag gcc															1440	
Ala	Cys	Asp	Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	
465				470						475				480		
agg gtg gtt ccg ggc cg ^g atc tgc ctg gac ctc gcc atc ctg gat															1488	
Arg	Val	Val	Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	
485					490					495						
agt gcc ttc ctg ctg tcc cag gtg gcc cca tcc ctg ttt atg ggc tcc															1536	
Ser	Ala	Phe	Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	
500					505					510						
att gtc cag ctc agc cag tct gtc act gcc tat atg gtg tct gcc gca															1584	
Ile	Val	Gln	Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	
515					520					525						
ggc ctg ggt ctg gtc gcc att tac ttt gct aca cag gta gta ttt gac															1632	
Gly	Leu	Gly	Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	
530					535					540						
aag agc gac ttg gcc aaa tac tca gcg tag															1662	
Lys	Ser	Asp	Leu	Ala	Lys	Tyr	Ser	Ala								
545					550											
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<211> 553																
<212> PRT																
<213> Homo sapiens																
<400> 13																
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala																
1				5					10				15			
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu																
				20					25				30			
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val																
				35					40				45			
Glu Glu Lys Phe Met Thr Val Leu Gly Ile Gly Pro Val Leu Gly																
				50					55				60			
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly																
				65					70				75			80
Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile																
				85					90				95			
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu																
				100					105				110			

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly
115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
420 425 430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
515 520 525

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
530 535 540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545 550